

SEQUENCE LISTING

<110> RHONE-POULENC AGRO
 <120> Method for increasing the content of cysteine, methionine,
 and glutathione in plants, and plants obtained
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 <150> FR9816163
 <151> 1998-12-17
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10		15							20					

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Asn	Phe	Arg	Phe	Pro	Gly	Phe	Ser	Val	Asn	Arg	Lys	Ile	His	His	Thr	
25									30		35				40	

caa	atc	gaa	gat	gac	gat	gtc	tgg	atc	aag	atg	ctt	gaa	gaa	gcc	198
Gln	Ile	Glu	Asp	Asp	Asp	Val	Trp	Ile	Lys	Met	Leu	Glu	Ala		
45									50			55			

aaa	tcc	gat	gtt	aaa	caa	gaa	ccc	att	tta	tca	aac	tac	tac	tac	gct	246
Lys	Ser	Asp	Val	Lys	Gln	Glu	Pro	Ile	Leu	Ser	Asn	Tyr	Tyr	Tyr	Ala	
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tcg	atc	aca	tct	cat	cga	tct	tta	gag	tct	gct	tta	gct	cac	atc	ctc	294
Ser	Ile	Thr	Ser	His	Arg	Ser	Leu	Glu	Ser	Ala	Leu	Ala	His	Ile	Leu	
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tcc	cta	aag	ctc	agg	aat	tta	aac	cta	cca	agc	aac	aca	ctc	tcc	gaa	342
Ser	Val	Lys	Leu	Ser	Asn	Leu	Asn	Leu	Pro	Ser	Asn	Thr	Leu	Phe	Glu	
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Leu	Phe	Ile	Ser	Val	Leu	Glu	Glu	Ser	Pro	Glu	Ile	Ile	Glu	Ser	Thr	
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Lys	Gln	Asp	Leu	Ile	Ala	Val	Lys	Glu	Arg	Asp	Pro	Ala	Cys	Ile	Ser	
125											130			135		

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 Tyr Val His Cys Phe Leu Gly Phe Lys Gly Phe Leu Ala Cys Gln Ala
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 cat cga ata gct cat acc ctc tgg aaa caq aac ags aaa atc gta gct 534
 His Arg Ile Ala His Thr Leu Trp Lys Gln Asn Arg Lys Ile Val Ala
 155 160 165

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 Leu Leu Ile Gln Asn Arg Val Ser Glu Ser Phe Ala Val Asp Ile His
 170 175 180

 ccc gga gcg aag atc gga aaa ggg att ctt tta gac cat gcg acg ggc 630
 Pro Gly Ala Lys Ile Gly Lys Gly Ile Leu Leu Asp His Ala Thr Gly
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 gtg gtg atc gga gaa acg gcg gtg gta gac aat gtt tcg att cta 678
 Val Val Ile Gly Glu Thr Ala Val Val Gly Asp Asn Val Ser Ile Leu
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 cac gga gtg acc ttg gga gga aca ggg aaa cag agt ggt gat cgg cat 726
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 220 225 230

 ccg aag att ggt gat ggt gtg ttg att gga gct ggg agt tgt ata ttg 774
 Pro Lys Ile Gly Asp Gly Val Leu Ile Gly Ala Gly Ser Cys Ile Leu
 235 240 245

 ggg aat ata aca atc ggt gaa gga gct aag att gga tca ggg tcg ttg 822
 Gly Asn Ile Thr Ile Gly Glu Gly Ala Lys Ile Gly Ser Gly Ser Val
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 Arg Leu Ile Gly Lys Glu Asn Pro Arg Lys His Asp Lys Ile Pro
 285 290 295

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 His Gln Ser Pro Ser Lys Glu Lys Leu Ser Ser Val Thr Gln Ser Asp
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gct gag gcg gag cca gct tta gct aac tat cta tat tcc acg att cct Ala Glu Ala Glu Pro Ala Leu Ala Ser Tyr Leu Tyr Ser Thr Ile Leu 60 65 70	246
tct cat tcg tct ctt gaa cga tct atc tcg tct cat cta gga aac aag Ser His Ser Ser Leu Glu Arg Ser Ile Ser Phe His Leu Gly Asn Lys 75 80 85	294
ctt tgt tcc tca acg ctt tca aca ctt tta tac gat ctg ttc tta Leu Cys Ser Ser Thr Leu Ieu Ser Thr Leu Leu Tyr Asp Leu Phe Leu 90 95 100	342
aac act tct tcc tcc gat cct tct cgt aac gcc acc gtc gca gat Asn Thr Phe Ser Ser Asp Pro Ser Leu Arg Asn Ala Thr Val Ala Asp 105 110 115 120	390
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tca cac aac cta tcg aca caa tca cgg aag cca tta gca tta gct cta Ser His Lys Leu Trp Thr Gin Ser Arg Lys Pro Leu Ala Leu Ala Leu 155 160 165	534
cac tca aca atc tcc gat gta ttc gct gtt gat att cat cca gca gcg His Ser Arg Ile Ser Asp Val Phe Ala Val Asp Ile His Pro Ala Ala 170 175 180	582
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gga gaa aca gca ggt att ggg aac aat gtt tca atc ctt cac cat gtg Gly Glu Thr Ala Val Ile Gly Asn Asn Val Ser Ile Leu His His Val 205 210 215	678
aca cta ggt gga aca ggt aaa gct tct gga gat aga cat ccg aac atc Thr Leu Gly Gly Thr Gly Lys Ala Cys Gly Asp Arg His Pro Lys Ile 220 225 230	726
ggc gac ggt tct ttg att gga gct gga gcg act att ctt gga aat gtc Gly Asp Gly Cys Leu Ile Gly Ala Gly Ala Thr Ile Leu Gly Asn Val 235 240 245	774
aag att ggt gca ggt gct aaa gta gga gct ggt tct gtt gtg ctg att Lys Ile Gly Ala Gly Ala Lys Val Gly Ala Gly Ser Val Val Leu Ile 250 255 260	822
gac gtc cct tct cgt ggt act gcg gtt ggg aat ccg gcg aca ctt gtc Asp Val Pro Cys Arg Gly Thr Ala Val Gly Asn Pro Ala Arg Leu Val 265 270 275 280	870

gga ggg aaa gag aag cca acg att cat gat gag gaa tgt cct gga gaa 918
 Gly Gly Lys Lys Pro Thr Ile His Asp Glu Glu Cys Pro Gly Glu
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 Arg Thr Gly Lys Pro Gln Ile Ser Pro Arg Asp Ser Ser Lys His His
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gac gat gaa tct ggc ttt cgt tac atg aac tcc tcc cgt tat cct gat 150
 Asp Asp Glu Ser Gly Phe Arg Tyr Met Asn Tyr Phe Arg Tyr Pro Asp
 25 30 35 40

cga tct tcc ttc aat gga acc cag acc aaa acc ctc cat act cgt cct 198
 Arg Ser Ser Phe Asn Gly Thr Gln Thr Lys Thr Leu His Thr Arg Pro
 45 50 55

ttg ctt gaa gat ctc gat cgc gac gct gaa gtc gat gat gtt tgg gcc 246
 Leu Leu Glu Asp Leu Asp Arg Asp Ala Glu Val Asp Asp Val Trp Ala
 60 65 70

aaa atc cga gaa gag gct aaa tct gat atc gcc aaa gaa cct att gtt 294
 Lys Ile Arg Glu Ala Lys Ser Asp Ile Ala Lys Glu Pro Ile Val
 75 80 85

tcc gct tat tat cac gct tcc att gtt tct cag cgt tcg ttg gaa gct 342
 Ser Ala Tyr Tyr His Ala Ser Ile Val Ser Gln Arg Ser Leu Glu Ala
 90 95 100

gcg ttg gcg aat act tta tct gtt aaa ctc agc aat ttg aat ctt cca 390
 Ala Leu Ala Asn Thr Leu Ser Val Lys Leu Ser Asn Leu Asn Leu Pro
 105 110 115 120

agc aac acg ctt ttc gat ttg ttc tct ggt gtt ctt caa gga aac cca 438
 Ser Asn Thr Leu Phe Asp Leu Phe Ser Gly Val Leu Gln Gly Asn Pro
 125 130 135

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 Asp Ile Val Glu Ser Val Lys Leu Asp Leu Leu Ala Val Lys Glu Arg
 140 145 150

gat cct gct tgt ata agc tac gtt cat tgt ttc ctt cac ttt aaa ggc 534
 Asp Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu His Phe Lys Gly
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tcc ctc gct tgc caa gcg cat cgt att gct cat gag ctt tgg act caq Phe Leu Ala Cys Gln Ala His Arg Ile Ala His Glu Leu Trp Thr Gin 170 175 180	582
gac aga aaa atc cta gct ttg ttg atc cag sac aga gtc tct gaa gca Asp Arg Lys Ile Leu Ala Leu Ile Gln Asn Arg Val Ser Glu Ala 185 190 195 200	630
tcc gct gtc gat tcc cac cct gga gct aac atc ggt acc ggg att ttg Phe Ala Val Asp Phe His Pro Gly Ala Lys Ile Gly Thr Gly Ile Leu 205 210 215	678
cta gac cat gct acg gct att ttg atc ggt gag acc gca gtt ttg ggg Leu Asp His Ala Thr Ala Ile Val Ile Gly Glu Thr Ala Val Val Gly 220 225 230	726
aac aat gtt tcg att ctc cat aac gtt acg ctt gga gga acc ggg aac Asn Asn Val Ser Ile Leu His Asn Val Thr Leu Gly Gly Thr Gly Lys 235 240 245	774
cag tgc gga gat agg cac ccc aag att ggc gat ggg gtt ttg att gga Gln Cys Gly Asp Arg His Pro Lys Ile Gly Asp Gly Val Leu Ile Gly 250 255 260	822
gct ggg aat tgc att ttg ggg aat atc acg att ggt gaa gga gct aag Ala Gly Thr Cys Ile Leu Gly Asn Ile Thr Ile Gly Glu Gly Ala Lys 265 270 275 280	870
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acg cat gac aag att cct ggc ttg act aac gac cag acg tcg cat ata Thr His Asp Lys Ile Pro Gly Leu Thr Met Asp Gln Thr Ser His Ile 315 320 325	1014
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His Phe Thr Met Ser Leu Tyr Met Leu Arg Ser Ser Pro His Ile
10 15 20

aat cat cac tct ttc ctt cct tct ttc gtt tcc tcc aaa ttc aaa Asn His His Ser Phe Leu Leu Pro Ser Phe Val Ser Ser Lys Phe Lys 25 30 35 40	150
cac cat act tta tct cct cct tct cct cct cct cct cct atg His His Thr Leu Ser Pro Pro Ser Pro Pro Pro Pro Pro Pro Met 45 50 55	198
gct gcg tgc atc gac acc tgc cgcc act ggt aaa ccc cag att tct cct Ala Ala Cys Ile Asp Thr Cys Arg Thr Gly Lys Pro Gln Ile Ser Pro 60 65 70	246
cgcc gat tct tct aaa cac cac gac gat gaa tct ggc ttt cgt tac atg Arg Asp Ser Ser Lys His His Asp Asp Glu Ser Gly Phe Arg Tyr Met 75 80 85	294
aac tac ttc cgt tat act gat cga tct tcc aat gga acc cag acc Asn Tyr Phe Arg Tyr Pro Asp Arg Ser Ser Phe Asn Gly Thr Gln Thr 90 95 100	342
aaa acc ctc cat act cgt cct ttg ctt gaa gat ctc gat cgcc gac gct Lys Thr Leu His Thr Arg Pro Leu Leu Glu Asp Leu Asp Arg Asp Ala 105 110 115 120	390
gaa gtc gat gat gtt tgg gcc aaa atc cga gaa gag gct aaa tct gat Glu Val Asp Asp Val Trp Ala Lys Ile Arg Glu Glu Ala Lys Ser Asp 125 130 135	438
atc gcs aaa gas cct att gtt tcc gct tat tat cac gct tcg att gtt Ile Ala Lys Glu Pro Ile Val Ser Ala Tyr Tyr His Ala Ser Ile Val 140 145 150	486
tct cag cgt tcg ttg gas gct ggc ttg gcg aat act tta tct gtt aaa Ser Gln Arg Ser Leu Glu Ala Ala Leu Ala Asn Thr Leu Ser Val Lys 155 160 165	534
ctc agc aat ttg aat ctt cca agc aac acg ctt ttc gat ttg tcc tct Leu Ser Asn Leu Asn Leu Pro Ser Asn Thr Leu Phe Asp Leu Phe Ser 170 175 180	582
ggt gtt ctt caa gga aac cca gat att gtt gaa tct gtc aag cta gat Gly Val Leu Gln Gly Asn Pro Asp Ile Val Glu Ser Val Lys Leu Asp 185 190 195 200	630
ctt tta gct gtt aag gag aga gat cct gct tgt ata agc tac gtt cat Leu Leu Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val His 205 210 215	678
tgt ttc ctt cac ttt aaa ggc ttc ctc gct tgt caa gcc cat cgt att Cys Phe Leu His Phe Lys Gly Phe Leu Ala Cys Gln Ala His Arg Ile 220 225 230	726
gct cat gag ctt tgg act cag gac aga aaa atc cta gct ttg ttg atc Ala His Glu Leu Trp Thr Gln Asp Arg Lys Ile Leu Ala Leu Ile 235 240 245	774
cag aac aga gtc tct gaa gcc ttc gct gtt gat ttc cac ccc gga gct Gln Asn Arg Val Ser Glu Ala Phe Ala Val Asp Phe His Pro Gly Ala 250 255 260	822
aaa acc ggt acc ggg att ttg cta gac cat gct acg gct att gtg atc Lys Ile Gly Thr Gly Ile Leu Leu Asp His Ala Thr Ala Ile Val Ile 265 270 275 280	870

ggt gag acg gcg gtt qtg ggg aac aat gtt tcg att ctc cat aac gtt 913
 Gly Glu Thr Ala Val Val Gly Asn Asn Val Ser Ile Leu His Asn Val
 285 290 295
 acg ctt gga gga acg ggg aaa cag tct gga gat agg cac ccg aag att 966
 Thr Leu Gly Gly Thr Gly Lys Gln Cys Gly Asp Arg His Pro Lys Ile
 300 305 310
 ggc gat ggg gtt ttg att gga gct ggg act tct att ttg ggg aat atc 1014
 Gly Asp Gly Val Leu Ile Gly Ala Gly Thr Cys Ile Leu Gly Asn Ile
 315 320 325
 acg att ggt gaa gga gct aag att ggt gcg ggg tcg qtg ttg aaa 1062
 Thr Ile Gly Glu Gly Ala Lys Ile Gly Ala Gly Ser Val Val Leu Lys
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 gac qtg ccg ccg cgt acg acg gct gtt gga aat ccg ccg aag ttg ctt 1110
 Asp Val Pro Pro Arg Thr Thr Ala Val Gly Asn Pro Ala Arg Leu Leu
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 ggt ggt aas gat aat ccg aas acg cat gac aag att cct ggt ttg act 1158
 Gly Gly Lys Asp Asn Pro Lys Thr His Asp Lys Ile Pro Gly Leu Thr
 365 370 375
 atg gac cag acg tcg cat ata tcc gag tgg tcg gat tat gta att 1203
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 Leu Ser Phe Val Gln Ser Lys Arg Val Cys Asp Ser Ser Leu Ser Ser
 20 25 30
 cct tgg aga gat atg aat ggc gat gag ctt ctc gag agt ggt ttc 144
 Pro Trp Arg Asp Met Asn Gly Asp Glu Leu Pro Phe Glu Ser Gly Phe
 35 40 45
 gag gtt tac gct aag gga act cat aag tca gag ttt gac tcg aat ttg 192
 Glu Val Tyr Ala Lys Gly Thr His Lys Ser Glu Phe Asp Ser Asn Leu
 50 55 60
 ctt gat cct tct gat cct att tgg gat gct ata aga gaa gaa gct 240
 Leu Asp Pro Arg Ser Asp Pro Ile Trp Asp Ala Ile Arg Glu Glu Ala
 65 70 75 80

aaa ctt gag gca gag aaa gag cct att ttg aqt agc ccc ttg tat get Lys Leu Glu Ala Glu Lys Glu Pro Ile Leu Ser Ser Phe Leu Tyr Ala 85 90 95	288
ggt atc tta gca cat gat tgt tta gag caa get tta ggg ttt gtt cta Gly Ile Leu Ala His Asp Cys Leu Glu Gln Ala Leu Gly Phe Val Leu 100 105 110	336
gcc aac cgt ctc caa aac cca acc ttg ttg gca aca caa ctc ttg qat Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Leu Asp 115 120 125	384
ata ttt tat ggt gtt atg atg cat gac aaa ggt att cag agt ttg att Ile Phe Tyr Gly Val Met His Asp Lys Gly Ile Gln Ser Ser Ile 130 135 140	432
ccg cat gat ctc cag gca ttt aaa gat cgt gat cct gct ttt ctt tcg Arg His Asp Leu Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu Ser 145 150 155 160	480
tat agt tct gct att tta cat ttg aag ggt tat cat gcg tta caa gca Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr His Ala Leu Gln Ala 165 170 175	528
tat agg gtt gcg cat aaa ctg tgg aat gaa ttt egg aaa cta tta gct Tyr Arg Val Ala His Lys Leu Trp Asn Glu Gly Arg Lys Leu Leu Ala 180 185 190	576
ctt gca ttg caa aac cga ata aqz gag gtt ttt ggc att gac ata cat Leu Ala Leu Gln Ser Arg Ile Ser Glu Val Phe Gly Ile Asp Ile His 195 200 205	624
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gtg gtc att ggt gag acc gct gtc ata ggc aac ggt gtc ttg att tta Val Val Ile Gly Glu Thr Ala Val Ile Gly Asn Gly Val Ser Ile Leu 225 230 235 240	720
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cca aag ata ggt gaa ggt gca ttg ctt gga gct ttt gtc act ata ctt Pro Lys Ile Gly Glu Gly Ala Leu Leu Gly Ala Cys Val Thr Ile Leu 260 265 270	816
ggg aac ata aac ata ggt gct gga gca atg gta gct gca ggt tca ctt Gly Asn Ile Ser Ile Gly Ala Gly Ala Met Val Ala Ala Gly Ser Leu 275 280 285	864
gtg tta aaa gag gtc ctt ttg cat aqt gtg gtg gct gga aat cct gca Val Leu Lys Asp Val Pro Ser His Ser Val Val Ala Gly Asn Pro Ala 290 295 300	912
aaa ctt atc agg gtc atg gaa gag caa gac ccg tct cta gca atq aaa Lys Leu Ile Arg Val Met Glu Glu Gln Asp Pro Ser Leu Ala Met Lys 305 310 315 320	960
cac gat gct act aaa gag ttc ttt cga cat gta gct gat ggt tac aaa His Asp Ala Thr Lys Glu Phe Phe Arg His Val Ala Asp Gly Tyr Lys 325 330 335	1008

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Gly Ala Gln Ser Asn Gly Pro Ser Leu Ser Ala Gly Asp Thr Glu Lys	
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10	15
ttg tct tct ctt cca arg att gtc tcc cgg aac ttt tct gcc aga gac	96
Leu Ser Ser Leu Pro Met Ile Val Ser Arg Asn Phe Ser Ala Arg Asp	
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gat gga gag acc ggt gac gag ttt cct ttc gag agg att ttc ccg gtt	144
Asp Gly Glu Thr Gly Asp Glu Phe Pro Phe Glu Arg Ile Phe Pro Val	
35	40
45	
tac gct aga gga acc ctt aat ccc gtg gcc gac ccg gtt ttg ctg gat	192
Tyr Ala Arg Gly Thr Leu Asn Pro Val Ala Asp Pro Val Leu Leu Asp	
50	55
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ttt acc aat tct agt tat gac cca att tgg gat tct ata aga gaa gaa	240
Phe Thr Asn Ser Ser Tyr Asp Pro Ile Trp Asp Ser Ile Arg Glu Glu	
65	70
75	80
gct aag ctt gag gca gaa gag gag ccg gtt ttg agt agc ttc ttg tat	288
Ala Lys Leu Ala Glu Glu Pro Val Leu Ser Ser Phe Leu Tyr	
85	90
95	
gct agt atc ttg tcg cat gac tgt tta gag caa gca ttg agt ttt gtt	336
Ala Ser Ile Leu Ser His Asp Cys Leu Glu Gln Ala Leu Ser Phe Val	
100	105
110	
cta gct aac cgt ctc caa aac cct acc ttg ttg gca act cag ctt atg	384
Leu Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Met	
115	120
125	
gat ata ttt tgc aac gtt atg gta cat gac aga ggt att caa agc tcc	432
Asp Ile Phe Cys Asn Val Met Val His Asp Arg Gly Ile Gln Ser Ser	
130	135
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att cgt ctt gat gtc cag gca ttc aaa gac aga gat cct gct tgt cta	480
Ile Arg Leu Asp Val Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu	
145	150
155	160
tcg tat agt tcc gct att tta cat ctg aag ggc tat ctt gca ctg cag	528
Ser Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr Leu Ala Leu Gln	
165	170
175	

gct tat aga gta gca cat aag ttg tgg aag caa gga aga aaa cca tta	576
Ala Tyr Arg Val Ala His Lys Leu Trp Lys Gln Gly Arg Lys Leu Leu	
180 185 190	
gca ttg gca ctg caa agc cga gta agc gag gta aga act gct gtg ata	624
Ala Leu Ala Leu Gin Ser Arg Val Ser Glu Val Arg Thr Ala Val Ile	
195 200 205	
ggc gac cgt gtc tca att ttg cat ggt gtg aca tta gga gga act ggg	672
Gly Asp Arg Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr Gly	
210 215 220	
aaa gaa acc ggt gac cgc cat cca aat ata ggc gac ggt gct ctt ctt	720
Lys Glu Thr Gly Asp Arg His Pro Asn Ile Gly Asp Gly Ala Leu Leu	
225 230 235 240	
gga gca tgt gtg act ata ctt ggt aac att aag ata ggc gct gga gca	768
Gly Ala Cys Val Thr Ile Leu Gly Asn Ile Lys Ile Gly Ala Gly Ala	
245 250 255	
atg gta gct gct ggt tcg ctt gtg tta aag gat gtt cct tcg cat agc	816
Met Val Ala Ala Gly Ser Leu Val Leu Lys Asp Val Pro Ser His Ser	
260 265 270	
atg gtg gct gga aat cca gca aaa ctc atc ggg ttt ctt gat gag caa	864
Met Val Ala Gly Asn Pro Ala Lys Leu Ile Gly Phe Val Asp Glu Gln	
275 280 285	
gat cca tct atg aca atg gag cat ggt gag tct tga	900
Asp Pro Ser Met Thr Met Glu His Gly Glu Ser	
290 295 300	
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gagagaggat ccttttcca atcataaaacc atggcaacat gcatacacac atgc	54
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<211> 53

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<223> Artificial sequence description:
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<211> 49

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<210> 15
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<400> 15
cctgtgtgat tgtcgtgtag tactctaga aactcgagaga gag 43

<210> 16
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tttttttt 67

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<400> 17
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